

0590
0620

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/977,261

DATE: 06/18/2002 P6
TIME: 09:12:20

Input Set : A:\38621259.app
Output Set: N:\CRF3\06182002\I977261.raw

3 <110> APPLICANT: ULLRICH, AXEL
4 GISHIZKY, MIKHAIL
5 SURES, IRMINGARD
7 <120> TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
9 <130> FILE REFERENCE: 038602/1259
11 <140> CURRENT APPLICATION NUMBER: 09/977,261
12 <141> CURRENT FILING DATE: 2001-10-16
14 <150> PRIOR APPLICATION NUMBER: 08/232,545
15 <151> PRIOR FILING DATE: 1994-04-22
17 <160> NUMBER OF SEQ ID NOS: 24
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2000
23 <212> TYPE: DNA
24 <213> ORGANISM: Unknown Organism
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (258)..(1778)
30 <220> FEATURE:
31 <223> OTHER INFORMATION: Description of Unknown Organism: Megakaryocyte
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34 <400> SEQUENCE: 1
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39 aggctcggtc cagtggcacc cagctcccta cctcctgtgc cagccgcctg gcctgtggca 180
41 ggccattccc agcgtccccg actgtgacca cttgctcagt gtgcctctca cctgcctcag 240
43 ttccctctg gggggcgc atg ggc ggg cga ggc tct ctg gtt tcc tgg cgg 290
44 Met Ala Gly Arg Gly Ser Leu Val Ser Trp Arg
45 1 5 10
47 gca ttt cac ggc tgt gat tct gct gag gaa ctt ccc cggtgtc agc ccc 338
48 Ala Phe His Gly Cys Asp Ser Ala Glu Glu Leu Pro Arg Val Ser Pro
49 15 20 25
51 cgc ttc ctc cga gcc tgg cac ccc cct ccc gtc tca gcc agg atg cca 386
52 Arg Phe Leu Arg Ala Trp His Pro Pro Pro Val Ser Ala Arg Met Pro
53 30 35 40
55 acg agg cgc tgg gcc ccg ggc acc cag tgt atc acc aaa tgc gag cac 434
56 Thr Arg Arg Trp Ala Pro Gly Thr Gln Cys Ile Thr Lys Cys Glu His
57 45 50 55
59 acc cgc ccc aag cca ggg gag ctg gcc ttc cgc aag ggc gac gtg gtc 482
60 Thr Arg Pro Lys Pro Gly Glu Leu Ala Phe Arg Lys Gly Asp Val Val
61 60 65 70 75
63 acc atc ctg gag gcc tgc gag aac aag agc tgg tac cgc gtc aag cac 530
64 Thr Ile Leu Glu Ala Cys Glu Asn Lys Ser Trp Tyr Arg Val Lys His

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Input Set : A:\38621259.app

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67	cac acc agt gga cag gag ggg ctg ctg gca gct ggg gcg ctg cgg gag			578
68	His Thr Ser Gly Gln Glu Gly Leu Leu Ala Ala Gly Ala Leu Arg Glu			
69	95	100	105	
71	cgg gag gcc ctc tcc gca gac ccc aag ctc agc ctc atg ccg tgg ttc			626
72	Arg Glu Ala Leu Ser Ala Asp Pro Lys Leu Ser Leu Met Pro Trp Phe			
73	110	115	120	
75	cac ggg aag atc tcg ggc cag gag gct gtc cag cag ctg cag cct ccc			674
76	His Gly Lys Ile Ser Gly Gln Glu Ala Val Gln Gln Leu Gln Pro Pro			
77	125	130	135	
79	gag gat ggg ctg ttc ctg gtg cgg gag tcc gcg cgc cac ccc ggc gac			722
80	Glu Asp Gly Leu Phe Leu Val Arg Glu Ser Ala Arg His Pro Gly Asp			
81	140	145	150	155
83	tac gtc ctg tgc gtg agc ttt ggc cgc gac gtc atc cac tac cgc gtg			770
84	Tyr Val Leu Cys Val Ser Phe Gly Arg Asp Val Ile His Tyr Arg Val			
85	160	165	170	
87	ctg cac cgc gac ggc cac ctc aca atc gat gag gcc gtg ttc ttc tgc			818
88	Leu His Arg Asp Gly His Leu Thr Ile Asp Glu Ala Val Phe Phe Cys			
89	175	180	185	
91	aac ctc atg gac atg gtg gag cat tac agc aag gac aag ggc gct atc			866
92	Asn Leu Met Asp Met Val Glu His Tyr Ser Lys Asp Lys Gly Ala Ile			
93	190	195	200	
95	tgc acc aag ctg gtg aga cca aag cgg aaa cac ggg acc aag tcg gcc			914
96	Cys Thr Lys Leu Val Arg Pro Lys Arg Lys His Gly Thr Lys Ser Ala			
97	205	210	215	
99	gag gag gag ctg gcc agg gcg ggc tgg tta ctg aac ctg cag cat ttg			962
100	Glu Glu Glu Leu Ala Arg Ala Gly Trp Leu Leu Asn Leu Gln His Leu			
101	220	225	230	235
103	aca ttg gga gca cag atc gga gag gga gag ttt gga gct gtc ctg cag			1010
104	Thr Leu Gly Ala Gln Ile Gly Glu Gly Glu Phe Gly Ala Val Leu Gln			
105	240	245	250	
107	ggt gag tac ctg ggg caa aag gtg gcc gtg aag aat atc aag tgt gat			1058
108	Gly Glu Tyr Leu Gly Gln Lys Val Ala Val Lys Asn Ile Lys Cys Asp			
109	255	260	265	
111	gtg aca gcc cag gcc ttc ctg gac gag acg gcc gtc atg acg aag atg			1106
112	Val Thr Ala Gln Ala Phe Leu Asp Glu Thr Ala Val Met Thr Lys Met			
113	270	275	280	
115	caa cac gag aac ctg gtg cgt ctc ctg ggc gtg atc ctg cac cag ggg			1154
116	Gln His Glu Asn Leu Val Arg Leu Leu Gly Val Ile Leu His Gln Gly			
117	285	290	295	
119	ctg tac att gtc atg gag cac gtg agc aag ggc aac ctg gtg aac ttt			1202
120	Leu Tyr Ile Val Met Glu His Val Ser Lys Gly Asn Leu Val Asn Phe			
121	300	305	310	315
123	ctg cgg acc cgg ggt cga gcc ctc gtg aac acc gct cag ctc ctg cag			1250
124	Leu Arg Thr Arg Gly Arg Ala Leu Val Asn Thr Ala Gln Leu Leu Gln			
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127	ttt tct ctg cac gtg gcc gag ggc atg gag tac ctg gag agc aag aag			1298
128	Phe Ser Leu His Val Ala Glu Gly Met Glu Tyr Leu Glu Ser Lys Lys			
129	335	340	345	

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131	ctt	gtg	cac	cgc	gac	ctg	gcc	cgc	aac	atc	ctg	gtc	tca	gag	gac	1346	
132	Leu	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu	Val	Ser	Glu	Asp	
133	350					355					360						
135	ctg	gtg	gcc	aag	gtc	agc	gac	ttt	ggc	ctg	gcc	aaa	gcc	gag	cgg	aag	1394
136	Leu	Val	Ala	Lys	Val	Ser	Asp	Phe	Gly	Leu	Ala	Lys	Ala	Glu	Arg	Lys	
137	365					370					375						
139	ggg	cta	gac	tca	agc	cgg	ctg	ccc	gtc	aag	tgg	acg	gcg	ccc	gag	gct	1442
140	Gly	Leu	Asp	Ser	Ser	Arg	Leu	Pro	Val	Lys	Trp	Thr	Ala	Pro	Glu	Ala	
141	380					385					390		395				
143	ctc	aaa	cac	ggg	aag	ttc	acc	agc	aag	tcg	gat	gtc	tgg	agt	ttt	ggg	1490
144	Leu	Lys	His	Gly	Lys	Phe	Thr	Ser	Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	
145	400					405					410						
147	gtg	ctg	ctc	tgg	gag	gtc	ttc	tca	tat	gga	cgg	gct	ccg	tac	cct	aaa	1538
148	Val	Leu	Leu	Trp	Glu	Val	Phe	Ser	Tyr	Gly	Arg	Ala	Pro	Tyr	Pro	Lys	
149	415					420					425						
151	atg	tca	ctg	aaa	gag	gtg	tcg	gag	gcc	gtg	gag	aag	ggg	tac	cgc	atg	1586
152	Met	Ser	Leu	Lys	Glu	Val	Ser	Glu	Ala	Val	Glu	Lys	Gly	Tyr	Arg	Met	
153	430					435					440						
155	gaa	ccc	ccc	gag	ggc	tgt	cca	ggc	ccc	gtg	cac	gtc	ctc	atg	agc	agc	1634
156	Glu	Pro	Pro	Glu	Gly	Cys	Pro	Gly	Pro	Val	His	Val	Leu	Met	Ser	Ser	
157	445					450					455						
159	tgc	tgg	gag	gca	gag	ccc	gcc	cgc	cgg	cca	ccc	ttc	cgc	aaa	ctg	gcc	1682
160	Cys	Trp	Glu	Ala	Glu	Pro	Ala	Arg	Arg	Pro	Pro	Phe	Arg	Lys	Leu	Ala	
161	460					465					470		475				
163	gag	aag	ctg	gcc	cgg	gag	cta	cgc	agt	gca	ggt	gcc	cca	gcc	tcc	gtc	1730
164	Glu	Lys	Leu	Ala	Arg	Glu	Leu	Arg	Ser	Ala	Gly	Ala	Pro	Ala	Ser	Val	
165	480					485					490						
167	tca	ggg	cag	gac	ggc	tcc	acc	tcg	ccc	cga	agc	cag	gag	ccc		1778	
168	Ser	Gly	Gln	Asp	Ala	Asp	Gly	Ser	Thr	Ser	Pro	Arg	Ser	Gln	Glu	Pro	
169	495					500					505						
171	tgaccccacc	cggtggggcc	cttggccca	gaggaccgag	agagtggaga	gtgcggcg	tg									1838	
173	ggggcaactga	ccaggcccaa	ggagggtcca	ggcgggcaag	tcatcctcct	gg	t	cccaca								1898	
175	gcaggggctg	ccccacgtag	ggggctctgg	gccccctgtg	gacacccca	ac	ct	gcgaag								1958	
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189	<400>	SEQUENCE:	2														
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193	Asp	Ser	Ala	Glu	Glu	Leu	Pro	Arg	Val	Ser	Pro	Arg	Phe	Leu	Arg	Ala	
194						20				25				30			
196	Trp	His	Pro	Pro	Pro	Val	Ser	Ala	Arg	Met	Pro	Thr	Arg	Arg	Trp	Ala	
197						35				40				45			
199	Pro	Gly	Thr	Gln	Cys	Ile	Thr	Lys	Cys	Glu	His	Thr	Arg	Pro	Lys	Pro	

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Input Set : A:\38621259.app
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202	Gly	Glu	Leu	Ala	Phe	Arg	Lys	Gly	Asp	Val	Val	Thr	Ile	Leu	Glu	Ala
203	65		70				75								80	
205	Cys	Glu	Asn	Lys	Ser	Trp	Tyr	Arg	Val	Lys	His	His	Thr	Ser	Gly	Gln
206							85			90					95	
208	Glu	Gly	Leu	Leu	Ala	Ala	Gly	Ala	Leu	Arg	Glu	Arg	Glu	Ala	Leu	Ser
209							100			105					110	
211	Ala	Asp	Pro	Lys	Leu	Ser	Leu	Met	Pro	Trp	Phe	His	Gly	Lys	Ile	Ser
212							115			120					125	
214	Gly	Gln	Glu	Ala	Val	Gln	Gln	Leu	Gln	Pro	Pro	Glu	Asp	Gly	Leu	Phe
215							130			135					140	
217	Leu	Val	Arg	Glu	Ser	Ala	Arg	His	Pro	Gly	Asp	Tyr	Val	Leu	Cys	Val
218	145						150			155					160	
220	Ser	Phe	Gly	Arg	Asp	Val	Ile	His	Tyr	Arg	Val	Leu	His	Arg	Asp	Gly
221							165			170					175	
223	His	Leu	Thr	Ile	Asp	Glu	Ala	Val	Phe	Phe	Cys	Asn	Leu	Met	Asp	Met
224							180			185					190	
226	Val	Glu	His	Tyr	Ser	Lys	Asp	Lys	Gly	Ala	Ile	Cys	Thr	Lys	Leu	Val
227							195			200					205	
229	Arg	Pro	Lys	Arg	Lys	His	Gly	Thr	Lys	Ser	Ala	Glu	Glu	Glu	Leu	Ala
230							210			215					220	
232	Arg	Ala	Gly	Trp	Leu	Leu	Asn	Leu	Gln	His	Leu	Thr	Leu	Gly	Ala	Gln
233	225						230			235					240	
235	Ile	Gly	Glu	Gly	Glu	Phe	Gly	Ala	Val	Leu	Gln	Gly	Glu	Tyr	Leu	Gly
236							245			250					255	
238	Gln	Lys	Val	Ala	Val	Lys	Asn	Ile	Lys	Cys	Asp	Val	Thr	Ala	Gln	Ala
239							260			265					270	
241	Phe	Leu	Asp	Glu	Thr	Ala	Val	Met	Thr	Lys	Met	Gln	His	Glu	Asn	Leu
242							275			280					285	
244	Val	Arg	Leu	Leu	Gly	Val	Ile	Leu	His	Gln	Gly	Leu	Tyr	Ile	Val	Met
245							290			295					300	
247	Glu	His	Val	Ser	Lys	Gly	Asn	Leu	Val	Asn	Phe	Leu	Arg	Thr	Arg	Gly
248	305						310			315					320	
250	Arg	Ala	Leu	Val	Asn	Thr	Ala	Gln	Leu	Leu	Gln	Phe	Ser	Leu	His	Val
251							325			330					335	
253	Ala	Glu	Gly	Met	Glu	Tyr	Leu	Glu	Ser	Lys	Lys	Leu	Val	His	Arg	Asp
254							340			345					350	
256	Leu	Ala	Ala	Arg	Asn	Ile	Leu	Val	Ser	Glu	Asp	Leu	Val	Ala	Lys	Val
257							355			360					365	
259	Ser	Asp	Phe	Gly	Leu	Ala	Lys	Ala	Glu	Arg	Lys	Gly	Leu	Asp	Ser	Ser
260							370			375					380	
262	Arg	Leu	Pro	Val	Lys	Trp	Thr	Ala	Pro	Glu	Ala	Leu	Lys	His	Gly	Lys
263	385						390			395					400	
265	Phe	Thr	Ser	Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	Leu	Leu	Trp	Glu
266							405			410					415	
268	Val	Phe	Ser	Tyr	Gly	Arg	Ala	Pro	Tyr	Pro	Lys	Met	Ser	Leu	Lys	Glu
269							420			425					430	
271	Val	Ser	Glu	Ala	Val	Glu	Lys	Gly	Tyr	Arg	Met	Glu	Pro	Pro	Glu	Gly
272							435			440					445	

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274 Cys Pro Gly Pro Val His Val Leu Met Ser Ser Cys Trp Glu Ala Glu
275 450 455 460
277 Pro Ala Arg Arg Pro Pro Phe Arg Lys Leu Ala Glu Lys Leu Ala Arg
278 465 470 475 480
280 Glu Leu Arg Ser Ala Gly Ala Pro Ala Ser Val Ser Gly Gln Asp Ala
281 485 490 495
283 Asp Gly Ser Thr Ser Pro Arg Ser Gln Glu Pro
284 500 505
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288 <211> LENGTH: 2500
289 <212> TYPE: DNA
290 <213> ORGANISM: Unknown Organism
292 <220> FEATURE:
293 <221> NAME/KEY: CDS
294 <222> LOCATION: (82)..(2106)
296 <220> FEATURE:
297 <223> OTHER INFORMATION: Description of Unknown Organism: Megakaryocyte
298 kinase 2
300 <400> SEQUENCE: 3
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303 agcgagtcta aggatgataa t atg gat aca aaa tct att cta gaa gaa ctt 111
304 Met Asp Thr Lys Ser Ile Leu Glu Glu Leu
305 1 5 10
307 ctt ctc aaa aga tca cag caa aag aag aaa atg tca cca aat aat tac 159
308 Leu Leu Lys Arg Ser Gln Gln Lys Lys Lys Met Ser Pro Asn Asn Tyr
309 15 20 25
311 aaa gaa cgg ctt ttt gtt ttg acc aaa aca aac ctt tcc tac tat gaa 207
312 Lys Glu Arg Leu Phe Val Leu Thr Lys Thr Asn Leu Ser Tyr Tyr Glu
313 30 35 40
315 tat gac aaa atg aaa agg ggc agc aga aaa gga tcc att gaa att aag 255
316 Tyr Asp Lys Met Lys Arg Gly Ser Arg Lys Gly Ser Ile Glu Ile Lys
317 45 50 55
319 aaa atc aga tgt gtg gag aaa gta aat ctc gag gag cag acg cct gta 303
320 Lys Ile Arg Cys Val Glu Lys Val Asn Leu Glu Glu Gln Thr Pro Val
321 60 65 70
323 gag aga cag tac cca ttt cag att gtc tat aaa gat ggg ctt ctc tat 351
324 Glu Arg Gln Tyr Pro Phe Gln Ile Val Tyr Lys Asp Gly Leu Leu Tyr
325 75 80 85 90
327 gtc tat gca tca aat gaa gag agc cga agt cag tgg ttg aaa gca tta 399
328 Val Tyr Ala Ser Asn Glu Glu Ser Arg Ser Gln Trp Leu Lys Ala Leu
329 95 100 105
331 caa aaa gag ata agg ggt aac ccc cac ctg ctg gtc aag tac cat agt 447
332 Gln Lys Glu Ile Arg Gly Asn Pro His Leu Leu Val Lys Tyr His Ser
333 110 115 120
335 ggg ttc ttc gtg gac ggg aag ttc ctg tgt tgc cag cag agc tgt aaa 495
336 Gly Phe Phe Val Asp Gly Lys Phe Leu Cys Cys Gln Gln Ser Cys Lys
337 125 130 135
339 gca gcc cca gga tgt acc ctc tgg gaa gca tat gct aat ctg cat act 543
340 Ala Ala Pro Gly Cys Thr Leu Trp Glu Ala Tyr Ala Asn Leu His Thr

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/18/2002
PATENT APPLICATION: US/09/977,261 TIME: 09:12:21

Input Set : A:\38621259.app
Output Set: N:\CRF3\06182002\I977261.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:20; N Pos. 14,20,23,26

Seq#:21; N Pos. 12,18,24

Seq#:24; Xaa Pos. 6

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/977,261

DATE: 06/18/2002

TIME: 09:12:21

Input Set : A:\38621259.app

Output Set: N:\CRF3\06182002\I977261.raw

L:2362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0

L:2389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0

L:2435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0